



Does Not Comply  
Corrected Diskette Needed

OIPE

**RAW SEQUENCE LISTING**  
PATENT APPLICATION: US/09/940,316B

DATE: 02/13/2003  
TIME: 13:57:40

Input Set : D:\30062-20026.txt  
Output Set: N:\CRF4\02132003\I940316B.raw

3 <110> APPLICANT: KOSAN BIOSCIENCES, Inc.  
 4 REEVES, CHRISTOPHER  
 5 CHU, DANIEL  
 6 KHOSLA, CHAITAN  
 7 SANTI, DANIEL  
 8 WU, KAI  
 10 <120> TITLE OF INVENTION: POLYKETIDES ENCODING THE fkbA GENE OF THE FK-520 POLYKETIDE  
 SYNTHASE  
 11 GENE CLUSTER  
 13 <130> FILE REFERENCE: 30062-20026.11  
 15 <140> CURRENT APPLICATION NUMBER: 09/940,316B  
 C--> 16 <141> CURRENT FILING DATE: 2003-02-05  
 18 <150> PRIOR APPLICATION NUMBER: 09/410,551  
 19 <151> PRIOR FILING DATE: 1999-10-01  
 21 <150> PRIOR APPLICATION NUMBER: US 60/139,650  
 22 <151> PRIOR FILING DATE: 1999-06-17  
 24 <150> PRIOR APPLICATION NUMBER: US 60/123,810  
 25 <151> PRIOR FILING DATE: 1999-03-11  
 27 <150> PRIOR APPLICATION NUMBER: US 60/102,748  
 28 <151> PRIOR FILING DATE: 1998-10-02  
 30 <160> NUMBER OF SEQ ID NOS: 72  
 32 <170> SOFTWARE: FastSEQ for Windows Version 4.0

#### ERRORED SEQUENCES

4615 <210> SEQ ID NO: 21  
 4616 <211> LENGTH: 1482  
 4617 <212> TYPE: PRT  
 4618 <213> ORGANISM: Artificial Sequence  
 4620 <220> FEATURE:  
 4621 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS  
 4622 synthase fragment  
 4624 <400> SEQUENCE: 21  
 4625 Gln Leu Ala Glu Ala Leu Leu Thr Leu Val Arg Glu Ser Thr Ala Ala  
 4626 1 5 10 15  
 4628 Val Leu Gly His Val Gly Gly Glu Asp Ile Pro Ala Thr Ala Ala Phe  
 4629 20 25 30  
 4631 Lys Asp Leu Gly Ile Asp Ser Leu Thr Ala Val Gln Leu Arg Asn Ala  
 4632 35 40 45  
 4634 Leu Thr Glu Ala Thr Gly Val Arg Leu Asn Ala Thr Ala Val Phe Asp  
 4635 50 55 60  
 4637 Phe Pro Thr Pro His Val Leu Ala Gly Lys Leu Gly Asp Glu Leu Thr  
 4638 65 70 75 80

Misalignment of amino  
numbering throughout. Only  
erroneous portion of sequence  
shown.

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4787 Ala Leu Ala His Leu Tyr Val Asn Gly Val Thr Val Asp Trp Pro Ala  
 4788 865 870 875 880  
 4790 Leu Leu Gly Asp Ala Pro Ala Thr Arg Val Leu Asp Leu Pro Thr Tyr  
 4791 885 890 895  
 4793 Ala Phe Gln His Gln Arg Tyr Trp Leu Glu Ser Ala Arg Pro Ala Ala  
 4794 900 905 910  
 4796 Ser Asp Ala Gly His Pro Val Leu Gly Ser Gly Ile Ala Leu Ala Gly  
 4797 915 920 925  
 4799 Ser Pro Gly Arg Val Phe Thr Gly Ser Val Pro Thr Gly Ala Asp Arg  
 4800 930 935 940  
 4802 Ala Val Phe Val Ala Glu Leu Ala Leu Ala Ala Asp Ala Val Asp  
 4803 945 950 955 960  
 4805 Cys Ala Thr Val Glu Arg Leu Asp Ile Ala Ser Val Pro Gly Arg Pro  
 4806 965 970 975  
 4808 Gly His Gly Arg Thr Thr Val Gln Thr Trp Val Asp Glu Pro Ala Asp  
 4809 980 985 990  
 4811 Asp Gly Arg Arg Arg Phe Thr Val His Thr Arg Thr Gly Asp Ala Pro  
 4812 995 1000 1005  
 4814 Trp Thr Leu His Ala Glu Gly Val Leu Arg Pro His Gly Thr Ala Leu  
 4815 1010 1015 1020  
 4817 Pro Asp Ala Ala Asp Ala Glu Trp Pro Pro Pro Gly Ala Val Pro Ala  
 4818 1025 1030 1035 1040  
 4820 Asp Gly Leu Pro Gly Val Trp Arg Arg Gly Asp Gln Val Phe Ala Glu  
 4821 1045 1050 1055  
 4823 Ala Glu Val Asp Gly Pro Asp Gly Phe Val Val His Pro Asp Leu Leu  
 4824 1060 1065 1070  
 4826 Asp Ala Val Phe Ser Ala Val Gly Asp Gly Ser Arg Gln Pro Ala Gly  
 4827 1075 1080 1085  
 4829 Trp Arg Asp Leu Thr Val His Ala Ser Asp Ala Thr Val Leu Arg Ala  
 4830 1090 1095 1100  
 4832 Cys Leu Thr Arg Arg Thr Asp Gly Ala Met Gly Phe Ala Ala Phe Asp  
 4833 1105 1110 1115 1120  
 4835 Gly Ala Gly Leu Pro Val Leu Thr Ala Glu Ala Val Thr Leu Arg Glu  
 4836 1125 1130 ← 1135  
 4838 Val Ala Ser Pro Ser Gly Ser Glu Glu Ser Asp Gly Leu His Arg Leu  
**E--> 4839 1140 1145 1150**  
 4841 Glu Trp Leu Ala Val Ala Glu Ala Val Tyr Asp Gly Asp Leu Pro Glu  
**E--> 4842 1155 1160 1165**  
 4844 Gly His Val Leu Ile Thr Ala Ala His Pro Asp Asp Pro Glu Asp Ile  
**E--> 4845 1170 1175 1180**  
 4847 Pro Thr Arg Ala His Thr Arg Ala Thr Arg Val Leu Thr Ala Leu Gln  
**E--> 4848 1185 1190 1195 1200**  
 4850 His His Leu Thr Thr Thr Asp His Thr Leu Ile Val His Thr Thr Thr  
**E--> 4851 1205 1210 ← 1215**  
 4853 Asp Pro Ala Gly Ala Thr Val Thr Gly Leu Thr Arg Thr Ala Gln Asn  
 4854 1220 1225 1230  
 4856 Glu His Pro His Arg Ile Arg Leu Ile Glu Thr Asp His Pro His Thr  
 4857 1235 1240 1245  
 4859 Pro Leu Pro Leu Ala Gln Leu Ala Thr Leu Asp His Pro His Leu Arg

Move to the left so that the last digit does not fall below the first letter of the next amino.

- Some

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Input Set : D:\30062-20026.txt

Output Set: N:\CRF4\02132003\I940316B.raw

4860	1250	1255	1260
4862	Leu Thr His His Thr Leu His His Pro His Leu Thr Pro Leu His Thr		
4863	1265	1270	1275
4865	1280		
4866	Thr Thr Pro Pro Thr Thr Pro Leu Asn Pro Glu His Ala Ile Ile		
4867	1285	1290	1295
4868	Ile Thr Gly Gly Ser Gly Thr Leu Ala Gly Ile Leu Ala Arg His Leu		
4869	1300	1305	1310
4871	Asn His Pro His Thr Tyr Leu Leu Ser Arg Thr Pro Pro Asp Ala		
4872	1315	1320	1325
4874	Thr Pro Gly Thr His Leu Pro Cys Asp Val Gly Asp Pro His Gln Leu		
4875	1330	1335	1340
4877	Ala Thr Thr Leu Thr His Ile Pro Gln Pro Leu Thr Ala Ile Phe His		
4878	1345	1350	1355
4880	1360		
4881	Thr Ala Ala Thr Leu Asp Asp Gly Ile Leu His Ala Leu Thr Pro Asp		
4883	1365	1370	1375
4884	Arg Leu Thr Thr Val Leu His Pro Lys Ala Asn Ala Ala Trp His Leu		
4885	1380	1385	1390
4886	His His Leu Thr Gln Asn Gln Pro Leu Thr His Phe Val Leu Tyr Ser		
4887	1395	1400	1405
4889	Ser Ala Ala Ala Val Leu Gly Ser Pro Gly Gln Gly Asn Tyr Ala Ala		
4890	1410	1415	1420
4892	Ala Asn Ala Phe Leu Asp Ala Leu Ala Thr His Arg His Thr Leu Gly		
4893	1425	1430	1435
4895	1440		
4896	Gln Pro Ala Thr Ser Ile Ala Trp Gly Met Trp His Thr Thr Ser Thr		
4898	1445	1450	1455
4899	Leu Thr Gly Gln Leu Asp Asp Ala Asp Arg Asp Arg Ile Arg Arg Gly		
4901	1460	1465	1470
4902	Gly Phe Leu Pro Ile Thr Asp Asp Glu Gly		
4902	1475	1480	
6722	<210> SEQ ID NO: 27		
6723	<211> LENGTH: 1557		
6724	<212> TYPE: PRT		
6725	<213> ORGANISM: Artificial Sequence		
6727	<220> FEATURE:		
6728	<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS		
6729	synthase fragment		
6731	<400> SEQUENCE: 27		
6732	Met Arg Leu Tyr Glu Ala Ala Arg Arg Thr Gly Ser Pro Val Val Val		
6733	1	5	10
6734	15		
6735	Ala Ala Ala Leu Asp Asp Ala Pro Asp Val Pro Leu Leu Arg Gly Leu		
6736	20	25	30
6737			
6738	Arg Arg Thr Thr Val Arg Arg Ala Ala Val Arg Glu Arg Ser Leu Ala		
6739	35	40	45
6741	Arg Arg Ser Pro Cys Cys Pro Thr Thr Ser Ala Pro Thr Pro Pro Ser		
6742	50	55	60
6744	Arg Ser Ser Trp Asn Ser Thr Ala Thr Val Leu Gly His Leu Gly Ala		
6745	65	70	75
6746	80		
6747	Glu Asp Ile Pro Ala Thr Thr Phe Lys Glu Leu Gly Ile Asp Ser		
6748	85	90	95

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Input Set : D:\30062-20026.txt

Output Set: N:\CRF4\02132003\I940316B.raw

6970 1265                    1270                    1275                    1280  
 6972 Val His Thr Thr Thr Asp Pro Pro Gly Ala Ala Val Thr Gly Leu Thr  
 6973                        1285                        1290                        1295  
 6975 Arg Thr Ala Gln Asn Glu His Pro Gly Arg Ile His Leu Ile Glu Thr  
 6976                        1300                        1305                        1310  
 6978 His His Pro His Thr Pro Leu Pro Leu Thr Gln Leu Thr Thr Leu His  
 6979                        1315                        1320                        1325  
 6981 Gln Pro His Leu Arg Leu Thr Asn Asn Thr Leu His Thr Pro His Leu  
 6982                        1330                        1335                        1340  
 6984 Thr Pro Ile Thr Thr His His Asn Thr Thr Thr Thr Pro Asn Thr  
 6985 1345                    1350                        1355                        1360  
 6987 Pro Pro Leu Asn Pro Asn His Ala Ile Leu Ile Thr Gly Gly Ser Gly  
 6988                        1365                        1370                        1375  
 6990 Thr Leu Ala Gly Ile Leu Ala Arg His Leu Asn His Pro His Thr Tyr  
 6991                        1380                        1385                        1390  
 6993 Leu Leu Ser Arg Thr Pro Pro Pro Pro Thr Thr Pro Gly Thr His Ile  
 6994                        1395                        1400                        1405  
 6996 Pro Cys Asp Leu Thr Asp Pro Thr Gln Ile Thr Gln Ala Leu Thr His  
 6997                        1410                        1415                        1420  
 6999 Ile Pro Gln Pro Leu Thr Gly Ile Phe His Thr Ala Ala Thr Leu Asp  
 E--> 7000 1~~425~~              ~~1430~~                    ~~1435~~                    1440                        - some  
 7002 Asp Ala Thr Leu Thr Asn Leu Thr Pro Gln His Leu Thr Thr Thr Leu  
 7003                        1445                        1450                        1455  
 7005 Gln Pro Lys Ala Asp Ala Ala Trp His Leu His His His Thr Gln Asn  
 7006                        1460                        1465                        1470  
 7008 Gln Pro Leu Thr His Phe Val Leu Tyr Ser Ser Ala Ala Ala Thr Leu  
 7009                        1475                        1480                        1485  
 7011 Gly Ser Pro Gly Gln Ala Asn Tyr Ala Ala Ala Asn Ala Phe Leu Asp  
 7012                        1490                        1495                        1500  
 7014 Ala Leu Ala Thr His Arg His Thr Gln Gly Gln Pro Ala Thr Thr Ile  
 7015 1505                    1510                        1515                        1520  
 7017 Ala Trp Gly Met Trp His Thr Thr Thr Thr Leu Thr Ser Gln Leu Thr  
 7018                        1525                        1530                        1535  
 7020 Asp Ser Asp Arg Asp Arg Ile Arg Arg Gly Gly Phe Leu Pro Ile Ser  
 7021                        1540                        1545                        1550  
 7023 Asp Asp Glu Gly Met  
 7024                        1555  
 8164 <210> SEQ ID NO: 31  
 8165 <211> LENGTH: 1578  
 8166 <212> TYPE: PRT  
 8167 <213> ORGANISM: Artificial Sequence  
 8169 <220> FEATURE:  
 8170 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS  
 8171                        synthase fragment  
 8173 <400> SEQUENCE: 31  
 8174 Met Arg Leu Tyr Glu Ala Ala Arg Arg Thr Gly Ser Pro Val Val Val  
 8175        1                5                        10                        15  
 8177 Ala Ala Ala Leu Asp Asp Ala Pro Asp Val Pro Leu Leu Arg Gly Leu  
 8178                        20                        25                            30

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Input Set : D:\30062-20026.txt

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8400	1205	1210	1215
8402	Gly Glu Val Ala Ser Ala Gly Gly Ser Asp Glu Ser Asp Gly Leu Leu		
8403	1220	1225	1230
8405	Arg Leu Glu Trp Leu Pro Val Ala Glu Ala His Tyr Asp Gly Ala Asp		
8406	1235	1240	1245
8408	Glu Leu Pro Glu Gly Tyr Thr Leu Ile Thr Ala Thr His Pro Asp Asp		
8409	1250	1255	1260
8411	Pro Asp Asp Pro Thr Asn Pro His Asn Thr Pro Thr Arg Thr His Thr		
8412	1265	1270	1275
8414	Gln Thr Thr Arg Val Leu Thr Ala Leu Gln His His Leu Ile Thr Thr		
8415	1285	1290	1295
8417	Asn His Thr Leu Ile Val His Thr Thr Asp Pro Pro Gly Ala Ala		
8418	1300	1305	1310
8420	Val Thr Gly Leu Thr Arg Thr Ala Gln Asn Glu His Pro Gly Arg Ile		
8421	1315	1320	1325
8423	His Leu Ile Glu Thr His His Pro His Thr Pro Leu Pro Leu Thr Gln		
8424	1330	1335	1340
8426	Leu Thr Thr Leu His Gln Pro His Leu Arg Leu Thr Asn Asn Thr Leu		
8427	1345	1350	1355
8429	His Thr Pro His Leu Thr Pro Ile Thr Thr His His Asn Thr Thr Thr		
8430	1365	1370	1375
8432	Thr Thr Pro Asn Thr Pro Pro Leu Asn Pro Asn His Ala Ile Leu Ile		
8433	1380	1385	1390
8435	Thr Gly Gly Ser Gly Thr Leu Ala Gly Ile Leu Ala Arg His Leu Asn		
8436	1395	1400	1405
8438	His Pro His Thr Tyr Leu Leu Ser Arg Thr Pro Pro Pro Pro Thr Thr		
8439	1410	1415	1420
8441	Pro Gly Thr His Ile Pro Cys Asp Leu Thr Asp Pro Thr Gln Ile Thr		
8442	1425	1430	1435
8444	Gln Ala Leu Thr His Ile Pro Gln Pro Leu Thr Gly Ile Phe His Thr		
8445	1445	1450	1455
8447	Ala Ala Thr Leu Asp Asp Ala Thr Leu Thr Asn Leu Thr Pro Gln His		
8448	1460	1465	1470
8450	Leu Thr Thr Leu Gln Pro Lys Ala Asp Ala Ala Trp His Leu His		
8451	1475	1480	1485
8453	His His Thr Gln Asn Gln Pro Leu Thr His Phe Val Leu Tyr Ser Ser		
8454	1490	1495	1500
8456	Ala Ala Ala Thr Leu Gly Ser Pro Gly Gln Ala Asn Tyr Ala Ala Ala		
8457	1505	1510	1515
8459	Asn Ala Phe Leu Asp Ala Leu Ala Thr His Arg His Thr Gln Gly Gln		
8460	1525	1530	1535
8462	Pro Ala Thr Thr Ile Ala Trp Gly Met Trp His Thr Thr Thr Leu		
E--> 8463	←1540	←1545	←1550
8465	Thr Ser Gln Leu Thr Asp Ser Asp Arg Asp Arg Ile Arg Arg Gly Gly		
8466	1555	1560	1565
8468	Phe Leu Pro Ile Ser Asp Asp Glu Gly Met		
8469	1570	1575	
8891	<210> SEQ ID NO: 33		
8892	<211> LENGTH: 1605		

- Some error

## RAW SEQUENCE LISTING

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Input Set : D:\30062-20026.txt

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8893 <212> TYPE: PRT  
 8894 <213> ORGANISM: Artificial Sequence  
 8896 <220> FEATURE:  
 8897 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS  
 8898 synthase fragment  
 8900 <400> SEQUENCE: 33

8901	Met	Arg	Leu	Tyr	Glu	Ala	Ala	Arg	Arg	Thr	Gly	Ser	Pro	Val	Val	Val
8902	1				5					10						15
8904	Ala	Ala	Ala	Leu	Asp	Asp	Ala	Pro	Asp	Val	Pro	Leu	Leu	Arg	Gly	Leu
8905				20				25							30	
8907	Arg	Arg	Thr	Thr	Val	Arg	Arg	Ala	Ala	Val	Arg	Glu	Arg	Ser	Leu	Ala
8908					35			40							45	
8910	Asp	Arg	Ser	Pro	Cys	Cys	Pro	Thr	Thr	Ser	Ala	Pro	Thr	Pro	Pro	Ser
8911		50					55				60					
8913	Arg	Ser	Ser	Trp	Asn	Ser	Thr	Ala	Thr	Val	Leu	Gly	His	Leu	Gly	Ala
8914	65				70				75						80	
8916	Glu	Asp	Ile	Pro	Ala	Thr	Thr	Thr	Phe	Lys	Glu	Leu	Gly	Ile	Asp	Ser
8917					85				90						95	
8919	Leu	Thr	Ala	Val	Gln	Leu	Arg	Asn	Ala	Leu	Thr	Thr	Ala	Thr	Gly	Val
8920					100				105						110	
8922	Arg	Leu	Asn	Ala	Thr	Ala	Val	Phe	Asp	Phe	Pro	Thr	Pro	Arg	Ala	Leu
8923					115			120							125	
8925	Ala	Ala	Arg	Leu	Gly	Asp	Glu	Leu	Ala	Gly	Thr	Arg	Ala	Pro	Val	Ala
8926		130				135				140						
8928	Ala	Arg	Thr	Ala	Ala	Thr	Ala	Ala	Ala	His	Asp	Glu	Pro	Leu	Ala	Ile
8929	145				150				155						160	
8931	Val	Gly	Met	Ala	Cys	Arg	Leu	Pro	Gly	Gly	Val	Ala	Ser	Pro	Gln	Glu
8932					165				170						175	
8934	Leu	Trp	Arg	Leu	Val	Ala	Ser	Gly	Thr	Asp	Ala	Ile	Thr	Glu	Phe	Pro
8935					180				185						190	
8937	Ala	Asp	Arg	Gly	Trp	Asp	Val	Asp	Ala	Leu	Tyr	Asp	Pro	Asp	Pro	Asp
8938		195				200				205						
8940	Ala	Ile	Gly	Lys	Thr	Phe	Val	Arg	His	Gly	Gly	Phe	Leu	Asp	Gly	Ala
8941		210				215				220						
8943	Thr	Gly	Phe	Asp	Ala	Ala	Phe	Phe	Gly	Ile	Ser	Pro	Arg	Glu	Ala	Leu
8944	225				230				235						240	
8946	Ala	Met	Asp	Pro	Gln	Gln	Arg	Val	Leu	Leu	Glu	Thr	Ser	Trp	Glu	Ala
8947					245				250						255	
8949	Phe	Glu	Ser	Ala	Gly	Ile	Thr	Pro	Asp	Ala	Ala	Arg	Gly	Ser	Asp	Thr
8950		260				265				270						
8952	Gly	Val	Phe	Ile	Gly	Ala	Phe	Ser	Tyr	Gly	Tyr	Gly	Thr	Gly	Ala	Asp
8953		275				280				285						
8955	Thr	Asn	Gly	Phe	Gly	Ala	Thr	Gly	Ser	Gln	Thr	Ser	Val	Leu	Ser	Gly
8956		290				295				300						
8958	Arg	Leu	Ser	Tyr	Phe	Tyr	Gly	Leu	Glu	Gly	Pro	Ser	Val	Thr	Val	Asp
8959	305				310				315						320	
8961	Thr	Ala	Cys	Ser	Ser	Ser	Leu	Val	Ala	Leu	His	Gln	Ala	Gly	Gln	Ser
8962			325				330				335					
8964	Leu	Arg	Ser	Gly	Glu	Cys	Ser	Leu	Ala	Leu	Val	Gly	Gly	Val	Thr	Val

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9186 Gln Pro Leu Thr His Phe Val Leu Tyr Ser Ser Ala Ala Ala Thr Leu  
 9187 1525 1530 1535  
 9189 Gly Ser Pro Gly Gln Ala Asn Tyr Ala Ala Ala Asn Ala Phe Leu Asp  
 9190 1540 1545 1550  
 9192 Ala Leu Ala Thr His Arg His Thr Gln Gly Gln Pro Ala Thr Thr Ile  
**E--> 9193** ←1555 ←1560 ←1565  
 9195 Ala Trp Gly Met Trp His Thr Thr Thr Leu Thr Ser Gln Leu Thr  
**E--> 9196** 1570 1575 1580  
 9198 Asp Ser Asp Arg Asp Arg Ile Arg Arg Gly Gly Phe Leu Pro Ile Ser  
**E--> 9199** 1585 1590 1595 1600  
 9201 Asp Asp Glu Gly Met  
**E--> 9202** 1605  
 9979 <210> SEQ ID NO: 72  
 9980 <211> LENGTH: 6396  
 9981 <212> TYPE: PRT  
 9982 <213> ORGANISM: Streptomyces hygroscopicus  
 9984 <400> SEQUENCE: 72  
 9985 Met Pro Glu Gln Asp Lys Thr Val Glu Tyr Leu Arg Trp Ala Thr Ala  
 9986 1 5 10 15  
 9987 Glu Leu Gln Lys Thr Arg Ala Glu Leu Ala Ala His Ser Glu Pro Leu  
 9988 20 25 30  
 9989 Ala Ile Val Gly Met Ala Cys Arg Leu Pro Gly Gly Val Ala Ser Pro  
 9990 35 40 45  
 9991 Glu Asp Leu Trp Gln Leu Leu Glu Ser Gly Gly Asp Gly Ile Thr Ala  
 9992 50 55 60  
 9993 Phe Pro Thr Asp Arg Gly Trp Glu Thr Thr Ala Asp Gly Arg Gly Gly  
 9994 65 70 75 80  
 9995 Phe Leu Thr Gly Ala Ala Gly Phe Asp Ala Ala Phe Phe Gly Ile Ser  
 9996 85 90 95  
 9997 Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg Leu Ala Leu Glu  
 9998 100 105 110  
 9999 Thr Ser Trp Glu Ala Phe Glu His Ala Gly Ile Asp Pro Gln Thr Leu  
 10000 115 120 125  
 10001 Arg Gly Ser Asp Thr Gly Val Phe Leu Gly Ala Phe Phe Gln Gly Tyr  
 10002 130 135 140  
 10003 Gly Ile Gly Ala Asp Phe Asp Gly Tyr Gly Thr Thr Ser Ile His Thr  
 10004 145 150 155 160  
 10005 Ser Val Leu Ser Gly Arg Leu Ala Tyr Phe Tyr Gly Leu Glu Gly Pro  
 10006 165 170 175  
 10007 Ala Val Thr Val Asp Thr Ala Cys Ser Ser Leu Val Ala Leu His  
 10008 180 185 190  
 10009 Gln Ala Gly Gln Ser Leu Arg Ser Gly Glu Cys Ser Leu Ala Leu Val  
 10010 195 200 205  
 10011 Gly Gly Val Thr Val Met Ala Ser Pro Ala Gly Phe Ala Asp Phe Ser  
 10012 210 215 220  
 10013 Glu Gln Gly Gly Leu Ala Pro Asp Ala Arg Cys Lys Ala Phe Ala Glu  
 10014 225 230 235 240  
 10015 Ala Ala Asp Gly Thr Gly Phe Ala Glu Gly Ser Gly Val Leu Ile Val  
 10016 245 250 255

amino number  
misaligned  
some

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Input Set : D:\30062-20026.txt

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10213 Leu Gly His Val Gly Gly Glu Asp Ile Pro Ala Thr Ala Ala Phe Lys  
 10214 1825 1830 1835 1840  
 10215 Asp Leu Gly Ile Asp Ser Leu Thr Ala Val Gln Leu Arg Asn Ala Leu  
 10216 1845 1850 1855  
 10217 Thr Glu Ala Thr Gly Val Arg Leu Asn Ala Thr Ala Val Phe Asp Phe  
 10218 1860 1865 1870  
 10219 Pro Thr Pro His Val Leu Ala Gly Lys Leu Gly Asp Glu Leu Thr Gly  
 10220 1875 1880 1885  
 10221 Thr Arg Ala Pro Val Val Pro Arg Thr Ala Ala Thr Ala Gly Ala His  
 10222 1890 1895 1900  
 10223 Asp Glu Pro Leu Ala Ile Val Gly Met Ala Cys Arg Leu Pro Gly Gly  
 10224 1905 1910 1915 1920  
 10225 Val Ala Ser Pro Glu Glu Leu Trp His Leu Val Ala Ser Gly Thr Asp  
 10226 1925 1930 1935  
 10227 Ala Ile Thr Glu Phe Pro Thr Asp Arg Gly Trp Asp Val Asp Ala Ile  
 10228 1940 1945 1950  
 10229 Tyr Asp Pro Asp Pro Asp Ala Ile Gly Lys Thr Phe Val Arg His Gly  
 10230 1955 1960 1965  
 10231 Gly Phe Leu Thr Gly Ala Thr Gly Phe Asp Ala Ala Phe Phe Gly Ile  
 10232 1970 1975 1980  
 10233 Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg Val Leu Leu  
 10234 1985 1990 1995 2000  
 10235 Glu Thr Ser Trp Glu Ala Phe Glu Ser Ala Gly Ile Thr Pro Asp Ser  
 10236 2005 2010 2015  
 10237 Thr Arg Gly Ser Asp Thr Gly Val Phe Val Gly Ala Phe Ser Tyr Gly  
 10238 2020 2025 2030  
 10239 Tyr Gly Thr Gly Ala Asp Thr Asp Gly Phe Gly Ala Thr Gly Ser Gln  
 10240 2035 2040 2045  
 10241 Thr Ser Val Leu Ser Gly Arg Leu Ser Tyr Phe Tyr Gly Leu Glu Gly  
 10242 2050 2055 2060  
 10243 Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu  
**E--> 10244 2065 2070 2075 2080 add**  
 10245 His Gln Ala Gly Gln Ser Leu Arg Ser Gly Glu Cys Ser Leu Ala Leu  
 10246 2085 2090 2095  
 10247 Val Gly Gly Val Thr Val Met Ala Ser Pro Gly Gly Phe Val Glu Phe  
 10248 2100 2105 2110  
 10249 Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg Ala Lys Ala Phe Gly  
 10250 2115 2120 2125  
 10251 Ala Gly Ala Asp Gly Thr Ser Phe Ala Glu Gly Ala Gly Val Leu Ile  
 10252 2130 2135 2140  
 10253 Val Glu Arg Leu Ser Asp Ala Glu Arg Asn Gly His Thr Val Leu Ala  
 10254 2145 2150 2155 2160  
 10255 Val Val Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu  
 10256 2165 2170 2175  
 10257 Ser Ala Pro Asn Gly Pro Ser Gln Glu Arg Val Ile Arg Gln Ala Leu  
 10258 2180 2185 2190  
 10259 Ala Asn Ala Gly Leu Thr Pro Ala Asp Val Asp Ala Val Glu Ala His  
 10260 2195 2200 2205  
 10261 Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu Ala Gln Ala Val Leu

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/940,316B

DATE: 02/13/2003

TIME: 13:57:42

Input Set : D:\30062-20026.txt

Output Set: N:\CRF4\02132003\I940316B.raw

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:2519 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:4839 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21  
M:332 Repeated in SeqNo=21  
L:7000 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27  
L:7351 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:28  
L:8463 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31  
L:9193 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:33  
M:332 Repeated in SeqNo=33  
L:10244 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:72